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(54) Title: MUTANT LUCIFERASES (57) Abstract The invention provides active, non-naturally occurring mutants of beetle luciferases and DNAs which encode such mutants. A mutant luciferase of the invention differs from the corresponding wild-type luciferase by producing bioluminescence with a wavelength of peak intensity that differs by at least 1 nm from the wavelength of peak intensity of the bioluminescence produced by the wild-type enzyme. The mutant luciferases and DNAs of the invention are employed in various biosensing applications.		

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MUTANT LUCIFERASES

TECHNICAL FIELD

This invention generally relates to luciferase enzymes that produce luminescence, like that from fireflies. More particularly, the invention concerns mutant luciferases of beetles. The mutant luciferases of the invention are made by genetic engineering, do not occur in nature, and, in each case, include modifications which cause a change in color in the luminescence that is produced. The luciferases of the invention can be used, like their naturally occurring counterparts, to provide luminescent signals in tests or assays for various substances or phenomena.

BACKGROUND OF THE INVENTION

The use of reporter molecules or labels to qualitatively or quantitatively monitor molecular events is well established. They are found in assays for medical diagnosis, for the detection of toxins and other substances in industrial environments, and for basic and applied research in biology, biomedicine, and biochemistry. Such assays include immunoassays, nucleic acid probe hybridization assays, and assays in which a reporter enzyme or other protein is produced by expression under control of a particular promoter. Reporter molecules, or labels in such assay systems, have included radioactive isotopes, fluorescent agents, enzymes and chemiluminescent agents.

Included in the assay system employing chemiluminescence to monitor or measure events of interest are assays which measure the activity of a bioluminescent enzyme, luciferase.

Light-emitting systems have been known and isolated from many luminescent organisms including bacteria, protozoa, coelenterates, molluscs, fish, millipedes, flies, fungi, worms, crustaceans, and beetles, particularly click beetles of genus *Pyrophorus* and the fireflies of the genera *Photinus*, *Photuris*, and

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Luciola. In many of these organisms, enzymes catalyze monooxygenations and utilize the resulting free energy to excite a molecule to a high energy state. Visible light is emitted when the excited molecule spontaneously
5 returns to the ground state. This emitted light is called "bioluminescence." Hereinafter it may also be referred to simply as "luminescence."

The limited occurrence of natural bioluminescence is an advantage of using luciferase enzymes as reporter
10 groups to monitor molecular events. Because natural bioluminescence is so rare, it is unlikely that light production from other biological processes will obscure the activity of a luciferase introduced into a biological system. Therefore, even in a complex environment, light
15 detection will provide a clear indication of luciferase activity.

Luciferases possess additional features which render them particularly useful as reporter molecules for biosensing (using a reporter system to reveal properties
20 of a biological system). Signal transduction in biosensors (sensors which comprise a biological component) generally involves a two step process: signal generation through a biological component, and signal transduction and amplification through an electrical component.
25 Signal generation is typically achieved through binding or catalysis. Conversion of these biochemical events into an electrical signal is typically based on electrochemical or caloric detection methods, which are limited by the free energy change of the biochemical
30 reactions. For most reactions this is less than the energy of hydrolysis for two molecules of ATP, or about 70 kJ/mole. However, the luminescence elicited by luciferases carries a much higher energy content. Photons emitted from the reaction catalyzed by firefly
35 luciferase (560 nm) have 214 KJ/einstein. Furthermore, the reaction catalyzed by luciferase is one of the most efficient bioluminescent reactions known, having a

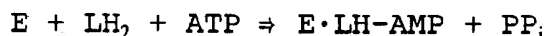
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quantum yield of nearly 0.9. This enzyme is therefore an extremely efficient transducer of chemical energy.

Since the earliest studies, beetle luciferases, particularly that from the common North American firefly species *Photinus pyralis*, have served as paradigms for understanding of bioluminescence. The fundamental knowledge and applications of luciferase have been based on a single enzyme, called "firefly luciferase," derived from *Photinus pyralis*. However, there are roughly 1800 species of luminous beetles worldwide. Thus, the luciferase of *Photinus pyralis* is a single example of a large and diverse group of beetle luciferases. It is known that all beetle luciferases catalyze a reaction of the same substrate, a polyheterocyclic organic acid, D-(-)-2-(6'-hydroxy-2'-benzothiazolyl)- Δ^2 -thiazoline-4-carboxylic acid (hereinafter referred to as "luciferin", unless otherwise indicated), which is converted to a high energy molecule. It is likely that the catalyzed reaction entails the same mechanism in each case.

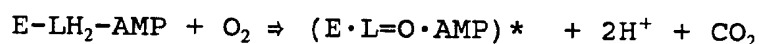
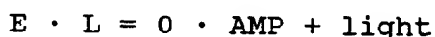
The general scheme involved in the mechanism of beetle bioluminescence appears to be one by which the production of light takes place after the oxidative decarboxylation of the luciferin, through interaction of the oxidized luciferin with the enzyme. The color of the light apparently is determined by the spatial organization of the enzyme's amino acids which interact with the oxidized luciferin.

The luciferase-catalyzed reaction which yields bioluminescence (hereinafter referred to simply as "the luciferase-luciferin reaction") has been described as a two-step process involving luciferin, adenosine triphosphate (ATP), and molecular oxygen. In the initial reaction, the luciferin and ATP react to form luciferyl adenylate with the elimination of inorganic pyrophosphate, as indicated in the following reaction:



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where E is the luciferase, LH_2 is luciferin, and PPi is pyrophosphate. The luciferyl adenylate, $\text{LH}_2\text{-AMP}$, remains tightly bound to the catalytic site of luciferase. When this form of the enzyme is exposed to molecular oxygen, the enzyme-bound luciferyl adenylate is oxidized to yield oxyluciferin ($\text{L}=\text{O}$) in an electronically excited state. The excited oxidized luciferin emits light on returning to the ground state as indicated in the following reaction:


$$\downarrow$$


One quantum of light is emitted for each molecule of luciferin oxidized. The electronically excited state of the oxidized luciferin is a characteristic state of the luciferase-luciferin reaction of a beetle luciferase; the color (and, therefore, the energy) of the light emitted upon return of the oxidized luciferin to the ground state is determined by the enzyme, as evidenced by the fact that various species of beetles having the same luciferin emit differently colored light.

Luciferases have been isolated directly from various sources. The cDNAs encoding luciferases of various beetle species have been reported. (See de Wet et al., *Molec. Cell. Biol.* 7, 725 - 737 (1987); Masuda et al., *Gene* 77, 265 - 270 (1989); Wood et al., *Science* 244, 700 - 702 (1989)). With the cDNA encoding a beetle luciferase in hand, it is entirely straightforward for the skilled to prepare large amounts of the luciferase by isolation from bacteria (e.g., *E. coli*), yeast, mammalian cells in culture, or the like, which have been transformed to express the cDNA. Alternatively, the cDNA, under control of an appropriate promoter and other

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signals for controlling expression, can be used in such a cell to provide luciferase, and ultimately bioluminescence catalyzed thereby, as a signal to indicate activity of the promoter. The activity of the promoter may, in turn, reflect another factor that is sought to be monitored, such as the concentration of a substance that induces or represses the activity of the promoter. Various cell-free systems, that have recently become available to make proteins from nucleic acids encoding them, can also be used to make beetle luciferases.

Further, the availability of cDNAs encoding beetle luciferases and the ability to rapidly screen for cDNAs that encode enzymes which catalyze the luciferase-luciferin reaction (see de Wet et al., supra and Wood et al., supra) also allow the skilled to prepare, and obtain in large amounts, other luciferases that retain activity in catalyzing production of bioluminescence through the luciferase-luciferin reaction. These other luciferases can also be prepared, and the cDNAs that encode them can also be used, as indicated in the previous paragraph. In the present disclosure, the term "beetle luciferase" or "luciferase" means an enzyme that is capable of catalyzing the oxidation of luciferin to yield bioluminescence, as outlined above.

The ready availability of cDNAs encoding beetle luciferases makes possible the use of the luciferases as reporters in assays employed to signal, monitor or measure genetic events associated with transcription and translation, by coupling expression of such a cDNA, and consequently production of the enzyme, to such genetic events.

Firefly luciferase has been widely used to detect promoter activity in eucaryotes. Though this enzyme has also been used in procaryotes, the utility of firefly luciferase as genetic reporter in bacteria is not commonly recognized. As genetic reporters, beetle

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luciferases are particularly useful since they are monomeric products of a single gene. In addition, no post-translational modifications are required for enzymatic activity, and the enzyme contains no prosthetic groups, bound cofactors, or disulfide bonds.

5 Luminescence from E.coli containing the gene for firefly luciferase can be triggered by adding the substrate luciferin to the growth medium. Luciferin readily penetrates biological membranes and cannot be used as a

10 carbon or nitrogen source by E.coli. The other substrates required for the bioluminescent reaction, oxygen and ATP, are available within living cells. However, measurable variations in luminescence color from luciferases would be needed for systems which utilize two

15 or more different luciferases as reporters (signal geneators).

Clones of different beetle luciferases, particularly of a single genus or species, can be utilized together in bioluminescent reporter systems.

20 Expression in exogenous hosts should differ little between these luciferases because of their close sequence similarity. Thus, in particular, the click beetle luciferases may provide a multiple reporter system that can allow the activity of two or more different promoters

25 to be monitored within a single host, or for different populations of cells to be observed simultaneously. The ability to distinguish each of the luciferases in a mixture, however, is limited by the width of their emissions spectra.

30 One of the most spectacular examples of luminescence color variation occurs in *Pyrophorus plagiophthalmus*, a large click beetle indigenous to the Caribbean. This beetle has two sets of light organs, a pair on the dorsal surface of the prothorax, and a single

35 organ in a ventral cleft of the abdomen. Four different luciferase clones have been isolated from the ventral organ. The luciferin-luciferase reactions catalyzed by

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these enzymes produces light that ranges from green to orange.

Spectral data from the luciferase-luciferin reaction catalyzed by these four luciferases show four overlapping peaks of nearly even spacing, emitting green (peak intensity: 546 nanometers), yellow-green (peak intensity: 560 nanometers), yellow (peak intensity: 578 nanometers) and orange (peak intensity: 593 nanometers) light. The respective proteins are named LucPplGR, LucPplYG, LucPplYE and LucPplOR. Though the wavelengths of peak intensity of the light emitted by these luciferases range over nearly 50 nm, there is still considerable overlap among the spectra, even those with peaks at 546 and 593 nm. Increasing the difference in wavelength of peak intensity would thus be useful to obtain greater measurement precision in systems using two or more luciferases.

The amino acid sequences of the four luciferases from the ventral organ are highly similar. Comparisons of the sequences show them to be 95 to 99% identical.

It would be desirable to enhance the utility of beetle luciferases for use in systems using multiple reporters to effect mutations in luciferase-encoding cDNAs to produce mutant luciferases which, in the luciferase-luciferin reaction, produce light with differences between wavelengths of peak intensity that are greater than those available using currently available luciferases.

Beetle luciferases are particularly suited for producing these mutant luciferases since color variation is a direct result of changes in the amino acid sequence.

Mutant luciferases of fireflies of genus *Luciola* are known in the art. Kajiyama et al., U.S. Patent Nos. 5,219,737 and 5,229,285.

In using luciferase expression in eukaryotic cells for biosensing, it would be desirable to reduce transport of the luciferase to peroxisomes. Sommer et

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al., Mol. Biol. Cell 3, 749 - 759 (1992), have described mutations in the three carboxy-terminal amino acids of *P. pyralis* luciferase that significantly reduce peroxisome-targeting of the enzyme.

5 The sequences of cDNAs encoding various beetle luciferases, and the amino acid sequences deduced from the cDNA sequences, are known, as indicated in Table I.

Table I

10 References for cDNA and Amino Acid Sequences of Various Wild-Type Beetle Luciferases

Luciferase	Reference
15 <i>LucPplGR</i>	K. Wood, Ph.D. Dissertation, University of California, San Diego (1989), see also SEQ ID NO:1; Wood et al., Science 244, 700-702 (1989)
20 <i>LucPplyG</i>	K. Wood, Ph.D. Dissertation, University of California, San Diego (1989); Wood et al., Science 244, 700-702 (1989)
25 <i>LucPplyE</i>	K. Wood, Ph.D. Dissertation, University of California, San Diego (1989); Wood et al., Science 244, 700-702 (1989)
30 <i>LucPplOR</i>	K. Wood, Ph.D. Dissertation, University of California, San Diego (1989); Wood et al., Science 244, 700-702 (1989)
35 <i>Photinus pyralis</i>	de Wet et al., Mol. Cell. Biol. 7, 725 - 737 (1987); K. Wood, Ph.D. Dissertation, University of California, San Diego (1989); Wood et al., Science 244, 700 - 702 (1989)
40 <i>Luciola cruciata</i>	Kajiyama et al., United States Patent No. 5,229,285; Masuda et al., United States Patent No. 4,968,613
45 <i>Luciola lateralis</i>	Kajiyama et al., United States Patent No. 5,229,285
50 <i>Luciola mingrelica</i>	Devine et al., Biochim. et Biophys. Acta 1173, 121-132(1993)

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The cDNA and amino acid sequences of LucPplGR, the green-emitting luciferase of the elaterid beetle *Pyrophorus plagiophthalmus*, are shown in SEQ ID NO:1.

5 SUMMARY OF THE INVENTION

The present invention provides mutant luciferases of beetles and DNAs which encode the mutant luciferases. Preferably, the mutant luciferases produce a light of different color from that of the corresponding wild-type
10 luciferase and preferably this difference in color is such that the wavelength of peak intensity of the luminescence of the mutant differs by at least 1 nm from that of the wild-type enzyme.

The mutant luciferases of the invention differ
15 from the corresponding wild-type enzymes by one or more, but typically fewer than three, amino acid substitutions. The luciferases of the invention may also entail changes in one or more of the three carboxy-terminal amino acids to reduce peroxisome targeting.

In one surprising aspect of the invention, it has
20 been discovered that combining in a single mutant two amino acid substitutions, each of which, by itself, occasions a change in color (shift in wavelength of peak intensity) of bioluminescence, causes the mutant to have
25 a shift in wavelength of peak intensity that is greater than either shift caused by the single amino acid substitutions.

cDNAs encoding the mutant luciferases of the invention may be obtained straightforwardly by any
30 standard, site-directed mutagenesis procedure carried out with a cDNA encoding the corresponding wild-type enzyme or another mutant. The mutant luciferases of the invention can be made by standard procedures for expressing the cDNAs which encode them in prokaryotic or
35 eukaryotic cells.

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A fuller appreciation of the invention will be gained upon examination of the following detailed description of the invention.

5 DETAILED DESCRIPTION OF THE INVENTION

In the following description and examples, process steps are carried out and concentrations are measured at room temperature (about 20 °C to 25 °C) and atmospheric pressure unless otherwise specified.

10 All amino acids referred to in the specification, except the non-enantiomorphous glycine, are L-amino acids unless specified otherwise. An amino acid may be referred to using the one-letter or three-letter designation, as indicated in the following Table II.

15

Table II

Designations for Amino Acids

Amino Acid	Three-Letter Designation	One-Letter Designation
20 L-alanine	Ala	A
L-arginine	Arg	R
L-asparagine	Asn	N
L-aspartic acid	Asp	D
L-cysteine	Cys	C
25 L-glutamic acid	Glu	E
L-glutamine	Gln	Q
glycine	Gly	G
L-histidine	His	H
L-isoleucine	Ile	I
30 L-leucine	Leu	L
L-lysine	Lys	K
L-methionine	Met	M
L-phenylalanine	Phe	F
L-proline	Pro	P
35 L-serine	Ser	S
L-threonine	Thr	T
L-tryptophan	Trp	W
L-tyrosine	Tyr	Y
L-valine	Val	V

40 "X" means any one of the twenty amino acids listed in Table II.

Peptide or polypeptide sequences are written and numbered from the initiating methionine, which is numbered "1," to the carboxy-terminal amino acid.

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A substitution at a position in a polypeptide is indicated with [designation for original amino acid]_[position number][designation for replacing amino acid]. For example, substitution of an alanine at position 100 in a polypeptide with a glutamic acid would be indicated by Ala₁₀₀Glu or A₁₀₀E. Typically, the substitution will be preceded by a designation for the polypeptide in which the substitution occurs. For example, if the substitution A₁₀₀E occurs in an hypothetical protein designated "Luck," the substitution would be indicated as Luck-Ala₁₀₀Glu or Luck-A₁₀₀E. If there is more than one substitution in a polypeptide, the indications of the substitutions are separated by slashes. For example, if the hypothetical protein "Luck" has a substitution of glutamic acid for alanine at position 100 and a substitution of asparagine for lysine at position 150, the polypeptide with the substitutions would be indicated as Luck-Ala₁₀₀Glu/Lys₁₅₀Asn or Luck-A₁₀₀E/K₁₅₀N. To indicate different substitutions at a position in a polypeptide, the designations for the substituting amino acids are separated by commas. For example, if the hypothetical "Luck" has substitutions of glutamic acid, glycine or lysine for alanine at position 100, the designation would be Luck-Ala₁₀₀/Glu,Gly,Lys or Luck-A₁₀₀/E,G,K.

The standard, one-letter codes "A," "C," "G," and "T" are used herein for the nucleotides adenylate, cytidylate, guanylate, and thymidylate, respectively. The skilled will understand that, in DNAs, the nucleotides are 2'-deoxyribonucleotide-5'-phosphates (or, at the 5'-end, triphosphates) while, in RNAs, the nucleotides are ribonucleotide-5'-phosphates (or, at the 5'-end, triphosphates) and uridylate (U) occurs in place of T. "N" means any one of the four nucleotides.

Oligonucleotide or polynucleotide sequences are written from the 5'-end to the 3'-end.

The term "mutant luciferase" is used herein to refer to a luciferase which is not naturally occurring

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and has an amino acid sequence that differs from those of naturally occurring luciferases.

In one of its aspects, the present invention is a mutant beetle luciferase which produces bioluminescence (i.e., catalyzes the oxidation of luciferin to produce bioluminescence) which has a shift in wavelength of peak intensity of at least 1 nm from the wavelength of peak intensity of the bioluminescence produced by the corresponding wild-type luciferase and has an amino acid sequence that differs from that of the corresponding wild-type luciferase by a substitution at one position or substitutions at two positions; provided that, if there is a substitution at one position, the position corresponds to a position in the amino acid sequence of LucPplGR selected from the group consisting of position 214, 215, 223, 224, 232, 236, 237, 238, 242, 244, 245, 247, 248, 282, 283 and 348; provided further that, if there are substitutions at two positions, at least one of the positions corresponds to a position in the amino acid sequence of LucPplGR selected from the group consisting of position 214, 215, 223, 224, 232, 236, 237, 238, 242, 244, 245, 247, 248, 282, 283 and 348; and provided that the mutant optionally has a peroxisome-targeting-avoiding sequence at its carboxy-terminus.

Exemplary mutant luciferases of the invention are those of the group consisting of LucPplGR-R₂₁₅H, -R₂₁₅G, -R₂₁₅T, -R₂₁₅M, -R₂₁₅P, -R₂₁₅A, -R₂₁₅L, -R₂₂₃L, -R₂₂₃Q, -R₂₂₃M, -R₂₂₃H, -V₂₂₄I, -V₂₂₄S, -V₂₂₄F, -V₂₂₄Y, -V₂₂₄L, -V₂₂₄H, -V₂₂₄G, -V₂₃₂E, -V₂₃₆H, -V₂₃₆W, -Y₂₃₇S, -Y₂₃₇C, -L₂₃₈R, -L₂₃₈M, -L₂₃₈Q, -L₂₃₈S, -L₂₃₈D, -H₂₄₂A, -F₂₄₄L, -G₂₄₅S, -G₂₄₅E, -S₂₄₇H, -S₂₄₇T, -S₂₄₇Y, -S₂₄₇F, -I₂₄₈R, -I₂₄₈V, -I₂₄₈F, -I₂₄₈T, -I₂₄₈S, -I₂₄₈N, -H₃₄₈N, -H₃₄₈Q, -H₃₄₈E, -H₃₄₈C, -S₂₄₇F/F₂₄₆L, -S₂₄₇F/I₂₄₈C, -S₂₄₇F/I₂₄₈T, -V₂₂₄F/R₂₁₅G, -V₂₂₄F/R₂₁₅T, -V₂₂₄F/R₂₁₅V, -V₂₂₄F/R₂₁₅P, -V₂₂₄F/P₂₂₂S, -V₂₂₄F/Q₂₂₇E, -V₂₂₄F/L₂₃₈V, -V₂₂₄F/L₂₃₈T, -V₂₂₄F/S₂₄₇G, -V₂₂₄F/S₂₄₇H, -V₂₂₄F/S₂₄₇T, and -V₂₂₄F/S₂₄₇F.

The following Table III shows spectral properties of these and other exemplary mutant luciferases.

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TABLE III

Protein		Spectral Properties		
	LucPplGR-	peak	shift	width
5	w.t.	545	0	72
	V ₂₁₄ S	*		
	Q	*		
	Y	*		
	K	*		
10	L	*		
	G	*		
	C	*		
	E	*		
	F	*		
15	P	*		
	H	*		
	R	*		
	R ₂₁₅ H	562	17	82
	Q	567	22	81
20	G	576	31	82
	T	576	31	84
	M	582	37	83
	P	588	43	91
	S	*		
25	Y	*		
	K	*		
	L	*		
	C	*		
	E	*		
30	F	*		
	R ₂₂₃ L	549	4	75
	Q	549	4	73

*Spectral shift (≥ 2 nm) observed by eye.

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TABLE III, cont.

Protein		Spectral Shift		
	LucPplGR-	peak	shift	width
5	R ₂₂₃ M	549	4	75
	H	551	6	75
	S	*		
	Y	*		
	K	*		
10	C	*		
	C	*		
	P	*		
	F	*		
	P	*		
15	V ₂₂₄ I	546	1	75
	S	556	11	74
	F	561	16	84
	Y	565	20	87
	L	578	33	94
20	H	584	39	69
	G	584	39	70
	V ₂₃₂ E	554	*	83
	V ₂₃₆ H	554	*	74
	W	554	9	74
25	Y ₂₃₇ S	553	1	73
	C	554	*	74
	L ₂₃₈ R	549	-1	72
	M	555	10	75
	Q	557	12	76
30	S	559	14	73
	D	568	23	76
	H ₂₄₂ A	559	14	75

*Spectral shift (≥ 2 nm) observed by eye.

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TABLE III, cont.

Protein		Spectral Properties		
	LucPplGR-	peak	shift	width
5	H ₂₄₂ S	561	16	74
	F ₂₄₄ L	555	19	74
	G ₂₄₅ S	558	19	75
	E	574	29	79
	S ₂₄₇ H	564	19	72
10	Y	566	21	79
	F	569	24	84
	I ₂₄₈ R	544	-1	72
	V	546	1	72
	F	548	3	74
15	T	554	9	75
	S	558	10	80
	N	577	32	80
	H ₃₄₈ A	592	47	67
	C	593	48	66
20	N	597	52	67
	Q	605	60	72
	V ₂₁₄ C/V ₂₂₄ A	559	14	72
	S ₂₄₇ F/F ₂₄₆ L	567	22	79
	S ₂₄₇ F/I ₂₄₈ C	586	44	84
25	S ₂₄₇ F/I ₂₄₈ T	596	51	80
	T ₂₃₃ A/L ₂₃₈ M	555	10	75
	V ₂₈₂ I/I ₂₈₃ V	563	3	73
	V ₂₂₄ F/R ₂₁₅ G	584	39	80
	V ₂₂₄ F/R ₂₁₅ T	587	42	80
30	V ₂₂₄ F/R ₂₁₅ V	589	44	80
	V ₂₂₄ F/R ₂₁₅ P	597	52	81
	V ₂₂₄ F/P ₂₂₂ S	564	3	86

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TABLE III, cont.

Protein	Spectral Properties		
LucPplGR-	peak	shift	width
V ₂₂₄ F/Q ₂₂₇ E	583	38	85
V ₂₂₄ F/L ₂₃₈ V	575	30	85
V ₂₂₄ F/L ₂₃₈ M	576	31	87
V ₂₂₄ F/S ₂₄₇ G	581	36	84
V ₂₂₄ F/S ₂₄₇ H	581	36	79
V ₂₂₄ F/S ₂₄₇ Y	595	50	88
V ₂₂₄ F/S ₂₄₇ F	597	52	85

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"Corresponding positions" in luciferases other than LucPplGR can be determined either from alignments at the amino acid level that are already known in the art (see, e.g., Wood et al., Science 244, 700 - 702 (1989);
5 Devine et al., Biochim. et Biophys. Acta 1173, 121-132(1993)) or by simply aligning at the amino acid level to maximize alignment of identical or conservatively substituted residues, and keeping in mind in particular that amino acids 195 - 205 in the LucPplGR sequence are
10 very highly conserved in all beetle luciferases and that there are no gaps for more than 300 positions after that highly conserved 11-mer in any beetle luciferase amino acid sequence.

A "peroxisome-targeting-avoiding sequence at its
15 carboxy-terminus" means (1) the three carboxy-terminal amino acids of the corresponding wild-type luciferase are entirely missing from the mutant; or (2) the three carboxy-terminal amino acids of the corresponding wild-type luciferase are replaced with a sequence, of one, two
20 or three amino acids that, in accordance with Sommer et al., supra, will reduce peroxisome-targeting by at least 50 %. If the three carboxy-terminal amino acids of the wild-type luciferase are replaced by a three-amino-acid peroxisome-targeting-avoiding sequence in the mutant, and
25 if the sequence in the mutant is $X_1X_2X_3$, where X_3 is carboxy-terminal, than X_1 is any of the twenty amino acids except A, C, G, H, N, P, Q, T and S, X_2 is any of the twenty amino acids except H, M, N, Q, R, S and K, and X_3 is any of the twenty amino acids except I, M, Y and L.
30 Further, any one or two, or all three, of X_1 , X_2 , and X_3 could be absent from the mutant (i.e., no amino acid corresponding to the position). The most preferred peroxisome-targeting-avoiding sequence is IAV, where V is at the carboxy-terminus.

35 In another of its aspects, the invention entails a combination of luciferases, in a cell (eukaryotic or prokaryotic), a solution (free or linked as a reporter to

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an antibody, antibody-fragment, nucleic acid probe, or the like), or adhered to a solid surface, optionally through an antibody, antibody fragment or nucleic acid, and exposed to a solution, provided that at least one of the luciferases is a mutant, both of the luciferases remain active in producing bioluminescence, and the wavelengths of peak intensities of the bioluminescence of the luciferases differ because the amino acid sequences of the luciferases differ at at least one of the positions corresponding to positions 214, 215, 223, 224, 232, 236, 237, 238, 242, 244, 245, 247, 248, 282, 283 and 348 in the amino acid sequence of LucPplGR, provided that one or both of the luciferases optionally have peroxisome-targeting-avoiding sequences.

In another of its aspects, the invention entails a DNA molecule, which may be an eukaryotic or prokaryotic expression vector, which comprises a segment which has a sequence which encodes a mutant beetle luciferase of the invention.

Most preferred among the DNAs of the invention are those with segments which encode a preferred mutant luciferase of the invention.

From the description of the invention provided herein, the skilled will recognize many modifications and variations of what has been described that are within the spirit of the invention. It is intended that such modifications and variations also be understood as part of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Promega Corporation
- (ii) TITLE OF INVENTION: Mutant Luciferases
- (iii) NUMBER OF SEQUENCES: 1
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Foley & Lardner
 - (B) STREET: P. O. Box 1497
 - (C) CITY: Madison
 - (D) STATE: Wisconsin
 - (E) COUNTRY: US
 - (F) ZIP: 53701-1497
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/177,081
 - (B) FILING DATE: 3-Jan-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Scanlon, William J.
 - (B) REGISTRATION NUMBER: 30136
 - (C) REFERENCE/DOCKET NUMBER: 19017/148P
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (608) 258-4284
 - (B) TELEFAX: (608) 258-4258

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1632 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTISENSE: no
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG ATG AAG AGA GAG AAA AAT GTT GTA TAT GGA CCC GAA CCC CTA CAC	48
Met Met Lys Arg Glu Lys Asn Val Val Tyr Gly Pro Glu Pro Leu His	
5 10 15	
CCC TTG GAA GAC TTA ACA GCA GGA GAA ATG CTC TTC AGG GCC CTT CGA	96
Pro Leu Glu Asp Leu Thr Ala Gly Glu Met Leu Phe Arg Ala Leu Arg	
20 25 30	
AAA CAT TCT CAT TTA CCG CAG GCT TTA GTA GAT GTG TAT GGT GAA GAA	144
Lys His Ser His Leu Pro Gln Ala Leu Val Asp Val Tyr Gly Glu Glu	
35 40 45	
TGG ATT TCA TAT AAA GAG TTT TTT GAA ACT ACA TGC CTA CTA GCA CAA	192
Trp Ile Ser Tyr Lys Glu Phe Phe Glu Thr Thr Cys Leu Leu Ala Gln	
50 55 60	
AGT CTT CAC AAT TGT GGA TAC AAG ATG AGT GAT GTA GTG TCG ATC TGC	240
Ser Leu His Asn Cys Gly Tyr Lys Met Ser Asp Val Val Ser Ile Cys	
65 70 75 80	
GCG GAG AAC AAT AAA AGA TTT TTT GTT CCC ATT ATT GCA GCT TGG TAT	288
Ala Glu Asn Asn Lys Arg Phe Phe Val Pro Ile Ile Ala Ala Trp Tyr	
85 90 95	
ATT GGT ATG ATT GTA GCA CCT GTT AAT GAG GGC TAC ATC CCA GAT GAA	336
Ile Gly Met Ile Val Ala Pro Val Asn Glu Gly Tyr Ile Pro Asp Glu	
100 105 110	
CTC TGT AAG GTC ATG GGT ATA TCG AGA CCA CAA CTA GTT TTT TGT ACA	384
Leu Cys Lys Val Met Gly Ile Ser Arg Pro Gln Leu Val Phe Cys Thr	
115 120 125	

AAG Lys	AAT Asn	ATT Ile	CTA Leu	AAT Asn	AAG Lys	GTA Val	TTG Leu	GAG Glu	GTA Val	CAG Gln	AGC Ser	AGA Arg	ACT Thr	GAT Asp	TTC Phe	432
130						135					140					
ATA Ile	AAA Lys	AGG Arg	ATT Ile	ATC Ile	ATA Ile	CTA Leu	GAT Asp	GCT Ala	GTA Val	GAA Glu	AAC Asn	ATA Ile	CAC His	GGT Gly	TGT Cys	480
145						150				155					160	
GAA Glu	AGT Ser	CTT Leu	CCC Pro	AAT Asn	TTT Phe	ATT Ile	TCT Ser	CGT Arg	TAT Tyr	TCG Ser	GAT Asp	GGA Gly	AAT Asn	ATT Ile	GCC Ala	528
				165					170					175		
AAC Asn	TTC Phe	AAA Lys	CCT Pro	TTA Leu	CAT His	TAC Tyr	GAT Asp	CCT Pro	GTT Val	GAA Glu	CAA Gln	GTG Val	GCA Ala	GCT Ala	ATC Ile	576
			180					185					190			
TTA Leu	TGT Cys	TCG Ser	TCA Ser	GGC Gly	ACA Thr	ACT Thr	GGA Gly	TTA Leu	CCG Pro	AAA Lys	GGT Gly	GTA Val	ATG Met	CAA Gln	ACT Thr	624
		195					200					205				
CAT His	AGA Arg	AAT Asn	GTT Val	TGT Cys	GTC Val	CGA Arg	CTT Leu	ATA Ile	CAT His	GCT Ala	TTA Leu	GAC Asp	CCC Pro	AGG Arg	GTA Val	672
	210					215					220					
GGA Gly	ACG Thr	CAA Gln	CTT Leu	ATT Ile	CCT Pro	GGT Gly	GTG Val	ACA Thr	GTC Val	TTA Leu	GTA Val	TAT Tyr	CTG Leu	CCT Pro	TTT Phe	720
225					230					235					240	
TTC Phe	CAT His	GCT Ala	TTT Phe	GGG Gly	TTC Phe	TCT Ser	ATA Ile	AAC Asn	TTG Leu	GGA Gly	TAC Tyr	TTC Phe	ATG Met	GTG Val	GGT Gly	768
				245				250					255			
CTT Leu	CGT Arg	GTT Val	ATC Ile	ATG Met	TTA Leu	AGA Arg	CGA Arg	TTT Phe	GAT Asp	CAA Gln	GAA Glu	GCA Ala	TTT Phe	CTA Leu	AAA Lys	816
			260					265					270			
GCT Ala	ATT Ile	CAG Gln	GAT Asp	TAT Tyr	GAA Glu	GTT Val	CGA Arg	AGT Ser	GTA Val	ATT Ile	AAC Asn	GTT Val	CCA Pro	GCA Ala	ATA Ile	864
		275					280					285				
ATA Ile	TTG Leu	TTC Phe	TTA Leu	TCG Ser	AAA Lys	AGT Ser	CCT Pro	TTG Leu	GTT Val	GAC Asp	AAA Lys	TAC Tyr	GAT Asp	TTA Leu	TCA Ser	912
	290					295					300					
AGT Ser	TTA Leu	AGG Arg	GAA Glu	TTG Leu	TGT Cys	TGC Cys	GGT Gly	GCG Ala	GCA Ala	CCA Pro	TTA Leu	GCA Ala	AAG Lys	GAA Glu	GTT Val	960
305					310					315					320	
GCT Ala	GAG Glu	ATT Ile	GCA Ala	GTA Val	AAA Lys	CGA Arg	TTA Leu	AAC Asn	TTG Leu	CCA Pro	GGA Gly	ATT Ile	CGC Arg	TGT Cys	GGA Gly	1008
				325					330					335		
TTT Phe	GGT Gly	TTG Leu	ACA Thr	GAA Glu	TCT Ser	ACT Thr	TCA Ser	GCT Ala	AAT Asn	ATA Ile	CAC His	AGT Ser	CTT Leu	AGG Arg	GAT Asp	1056
			340					345					350			
GAA Glu	TTT Phe	AAA Lys	TCA Ser	GGA Gly	TCA Ser	CTT Leu	GGA Gly	AGA Arg	GTT Val	ACT Thr	CCT Pro	TTA Leu	ATG Met	GCA Ala	GCT Ala	1104
		355					360					365				
AAA Lys	ATA Ile	GCA Ala	GAT Asp	AGG Arg	GAA Glu	ACT Thr	GGT Gly	AAA Lys	GCA Ala	TTG Leu	GGA Gly	CCA Pro	AAT Asn	CAA Gln	GTT Val	1152
	370					375					380					
GGT Gly	GAA Glu	TTA Leu	TGC Cys	ATT Ile	AAA Lys	GGT Gly	CCC Pro	ATG Met	GTA Val	TCG Ser	AAA Lys	GGT Gly	TAC Tyr	GTG Val	AAC Asn	1200
385					390					395					400	

AAT	GTA	GAA	GCT	ACC	AAA	GAA	GCT	ATT	GAT	GAT	GAT	GGT	TGG	CTT	CAC	1248
Asn	Val	Glu	Ala	Thr	Lys	Glu	Ala	Ile	Asp	Asp	Asp	Gly	Trp	Leu	His	
				405					410					415		
TCT	GGA	GAC	TTT	GGA	TAC	TAT	GAT	GAG	GAT	GAG	CAT	TTC	TAT	GTG	GTG	1296
Ser	Gly	Asp	Phe	Gly	Tyr	Tyr	Asp	Glu	Asp	Glu	His	Phe	Tyr	Val	Val	
			420					425					430			
GAC	CGT	TAC	AAG	GAA	TTG	ATT	AAA	TAT	AAG	GGC	TCT	CAG	GTA	GCA	CCT	1344
Asp	Arg	Tyr	Lys	Glu	Leu	Ile	Lys	Tyr	Lys	Gly	Ser	Gln	Val	Ala	Pro	
			435				440					445				
GCA	GAA	CTA	GAA	GAG	ATT	TTA	TTG	AAA	AAT	CCA	TGT	ATC	AGA	GAT	GTT	1392
Ala	Glu	Leu	Glu	Glu	Ile	Leu	Leu	Lys	Asn	Pro	Cys	Ile	Arg	Asp	Val	
	450					455					460					
GCT	GTG	GTT	GGT	ATT	CCT	GAT	CTA	GAA	GCT	GGA	GAA	CTG	CCA	TCT	GCG	1440
Ala	Val	Val	Gly	Ile	Pro	Asp	Leu	Glu	Ala	Gly	Glu	Leu	Pro	Ser	Ala	
	465				470					475					480	
TTT	GTG	GTT	ATA	CAG	CCC	GGA	AAG	GAG	ATT	ACA	GCT	AAA	GAA	GTT	TAC	1488
Phe	Val	Val	Ile	Gln	Pro	Gly	Lys	Glu	Ile	Thr	Ala	Lys	Glu	Val	Tyr	
			485						490					495		
GAT	TAT	CTT	GCC	GAG	AGG	GTC	TCC	CAT	ACA	AAG	TAT	TTG	CGT	GGA	GGG	1536
Asp	Tyr	Leu	Ala	Glu	Arg	Val	Ser	His	Thr	Lys	Tyr	Leu	Arg	Gly	Gly	
			500					505					510			
GTT	CGA	TTC	GTT	GAT	AGC	ATA	CCA	AGG	AAT	GTT	ACA	GGT	AAA	ATT	ACA	1584
Val	Arg	Phe	Val	Asp	Ser	Ile	Pro	Arg	Asn	Val	Thr	Gly	Lys	Ile	Thr	
		515					520					525				
AGA	AAG	GAA	CTT	CTG	AAG	CAG	TTG	CTG	GAG	AAG	AGT	TCT	AAA	CTT	TAA	1632
Arg	Lys	Glu	Leu	Leu	Lys	Gln	Leu	Leu	Glu	Lys	Ser	Ser	Lys	Leu		
	530					535					540					

CLAIMS

1. A mutant beetle luciferase which has an amino acid sequence that differs from that of the corresponding wild-type luciferase by a substitution at one position or
5 substitutions at two positions; provided that, if there is a substitution at one position, the position corresponds to a position in the amino acid sequence of LucPplGR selected from the group consisting of position 214, 215, 223, 224, 232, 236, 237, 238, 242, 244, 245,
10 247, 248, 282, 283 and 348; and provided further that, if there are substitutions at two positions, at least one of the positions corresponds to a position in the amino acid sequence of LucPplGR selected from the group consisting of position 214, 215, 223, 224, 232, 236, 237, 238, 242,
15 244, 245, 247, 248, 282, 283 and 348.

2. A mutant luciferase according to Claim 1 wherein there is one amino acid substitution.

3. A mutant luciferase according to Claim 1 wherein there are two amino acid substitutions.

20 4. A mutant luciferase according to Claim 3 wherein each of the amino acid substitutions is at a position corresponding to a position in the amino acid sequence of LucPplGR selected from the group consisting of position 214, 215, 223, 224, 232, 236, 237, 238, 242,
25 244, 245, 247, 248, 282, 283 and 348.

5. A mutant luciferase according to Claim 1 wherein the corresponding wild-type luciferase is selected from the group consisting of LucPplGR, LucPplYG, LucPplYE, LucPplOR, the luciferase of *Photinus pyralis*,
30 the luciferase of *Luciola cruciata*, the luciferase of *Luciola lateralis*, and the luciferase of *Luciola mingrelica*.

6. A mutant luciferase according to Claim 2 wherein the corresponding wild-type luciferase is selected from the group consisting of LucPplGR, LucPplyG, LucPplyE, LucPplOR, the luciferase of *Photinus pyralis*,
5 the luciferase of *Luciola cruciata*, the luciferase of *Luciola lateralis*, and the luciferase of *Luciola mingrelica*.

7. A mutant luciferase according to Claim 3 wherein the corresponding wild-type luciferase is
10 selected from the group consisting of LucPplGR, LucPplyG, LucPplyE, LucPplOR, the luciferase of *Photinus pyralis*, the luciferase of *Luciola cruciata*, the luciferase of *Luciola lateralis*, and the luciferase of *Luciola mingrelica*.

15 8. A mutant luciferase according to Claim 4 wherein the corresponding wild-type luciferase is selected from the group consisting of LucPplGR, LucPplyG, LucPplyE, LucPplOR, the luciferase of *Photinus pyralis*, the luciferase of *Luciola cruciata*, the luciferase of
20 *Luciola lateralis*, and the luciferase of *Luciola mingrelica*.

9. A mutant luciferase according to Claim 5 wherein the corresponding wild-type luciferase is selected from the group consisting of LucPplGR, LucPplyG,
25 LucPplyE, and LucPplOR.

10. A mutant luciferase according to Claim 6 wherein the corresponding wild-type luciferase is selected from the group consisting of LucPplGR, LucPplyG, LucPplyE, and LucPplOR.

30 11. A mutant luciferase according to Claim 7 wherein the corresponding wild-type luciferase is selected from the group consisting of LucPplGR, LucPplyG, LucPplyE, and LucPplOR.

12 A mutant luciferase according to Claim 8
35 wherein the corresponding wild-type luciferase is selected from the group consisting of LucPplGR, LucPplyG, LucPplyE, and LucPplOR.

13. A mutant luciferase of Claim 9 wherein the corresponding wild-type luciferase is LucPplGR.

14. A mutant luciferase of Claim 10 wherein the corresponding wild-type luciferase is LucPplGR.

5 15. A mutant luciferase of Claim 11 wherein the corresponding wild-type luciferase is LucPplGR.

16. A mutant luciferase of Claim 12 wherein the corresponding wild-type luciferase is LucPplGR.

10 17. A mutant luciferase of Claim 13 wherein the mutant is selected from the group consisting of
LucPplGR-R₂₁₅H, -R₂₁₅G, -R₂₁₅T, -R₂₁₅M, -R₂₁₅P, -R₂₁₅A, -R₂₁₅L,
-R₂₂₃L, -R₂₂₃Q, -R₂₂₃M, -R₂₂₃H, -V₂₂₄I, -V₂₂₄S, -V₂₂₄F, -V₂₂₄Y, -V₂₂₄L,
-V₂₂₄H, -V₂₂₄G, -V₂₃₂E, -V₂₃₆H, -V₂₃₆W, -Y₂₃₇S, -Y₂₃₇C, -L₂₃₈R, -L₂₃₈M,
-L₂₃₈Q, -L₂₃₈S, -L₂₃₈D, -H₂₄₂A, -F₂₄₄L, -G₂₄₅S, -G₂₄₅E, -S₂₄₇H, -S₂₄₇T,
15 -S₂₄₇Y, -S₂₄₇F, -I₂₄₈R, -I₂₄₈V, -I₂₄₈F, -I₂₄₈T, -I₂₄₈S, -I₂₄₈N, -H₃₄₈N,
-H₃₄₈Q, -H₃₄₈E, -H₃₄₈C, -S₂₄₇F/F₂₄₆L, -S₂₄₇F/I₂₄₈C, -S₂₄₇F/I₂₄₈T,
-V₂₂₄F/R₂₁₅G, -V₂₂₄F/R₂₁₅T, -V₂₂₄F/R₂₁₅V, -V₂₂₄F/R₂₁₅P, -V₂₂₄F/P₂₂₂S,
-V₂₂₄F/Q₂₂₇E, -V₂₂₄F/L₂₃₈V, -V₂₂₄F/L₂₃₈T, -V₂₂₄F/S₂₄₇G, -V₂₂₄F/S₂₄₇H,
-V₂₂₄F/S₂₄₇T, and -V₂₂₄F/S₂₄₇F.

20 18. A DNA molecule which comprises a segment which has a sequence which encodes a mutant beetle luciferase which has an amino acid sequence that differs from that of the corresponding wild-type luciferase by a substitution at one position or substitutions at two
25 positions; provided that, if there is a substitution at one position, the position corresponds to a position in the amino acid sequence of LucPplGR selected from the group consisting of position 214, 215, 223, 224, 232, 236, 237, 238, 242, 244, 245, 247, 248, 282, 283 and 348;
30 and provided further that, if there are substitutions at two positions, at least one of the positions corresponds to a position in the amino acid sequence of LucPplGR selected from the group consisting of position 214, 215, 223, 224, 232, 236, 237, 238, 242, 244, 245, 247, 248,
35 282, 283 and 348.

19. A DNA molecule according to Claim 18 wherein the encoded mutant luciferase has one amino acid substitution.

20. A DNA molecule according to Claim 18 wherein
5 the encoded mutant luciferase has two amino acid substitutions.

21. A DNA molecule according to Claim 20 wherein, in the encoded mutant luciferase, each of the amino acid substitutions is at a position corresponding to a
10 position in the amino acid sequence of LucPplGR selected from the group consisting of position 214, 215, 223, 224, 232, 236, 237, 238, 242, 244, 245, 247, 248, 282, 283 and 348.

22. A DNA molecule according to Claim 18 wherein,
15 for the encoded amino acid sequence, the corresponding wild-type luciferase is selected from the group consisting of LucPplGR, LucPplyG, LucPplyE, LucPplOR, the luciferase of *Photinus pyralis*, the luciferase of *Luciola cruciata*, the luciferase of *Luciola lateralis*, and the
20 luciferase of *Luciola mingrelica*.

23. A DNA molecule according to Claim 19 wherein, for the encoded amino acid sequence, the corresponding wild-type luciferase is selected from the group consisting of LucPplGR, LucPplyG, LucPplyE, LucPplOR, the
25 luciferase of *Photinus pyralis*, the luciferase of *Luciola cruciata*, the luciferase of *Luciola lateralis*, and the luciferase of *Luciola mingrelica*.

24. A DNA molecule according to Claim 20 wherein, for the encoded amino acid sequence, the corresponding
30 wild-type luciferase is selected from the group consisting of LucPplGR, LucPplyG, LucPplyE, LucPplOR, the luciferase of *Photinus pyralis*, the luciferase of *Luciola cruciata*, the luciferase of *Luciola lateralis*, and the luciferase of *Luciola mingrelica*.

25. A DNA molecule according to Claim 21 wherein,
for the encoded amino acid sequence, the corresponding
wild-type luciferase is selected from the group
consisting of LucPplGR, LucPplyG, LucPplyE, LucPplOR, the
5 luciferase of *Photinus pyralis*, the luciferase of *Luciola
cruciata*, the luciferase of *Luciola lateralis*, and the
luciferase of *Luciola mingrelia*.

26. A DNA molecule according to Claim 22 wherein,
for the encoded amino acid sequence, the corresponding
10 wild-type luciferase is selected from the group
consisting of LucPplGR, LucPplyG, LucPplyE, and LucPplOR.

27. A mutant luciferase according to Claim 23
wherein, for the encoded amino acid sequence, the
corresponding wild-type luciferase is selected from the
15 group consisting of LucPplGR, LucPplyG, LucPplyE, and
LucPplOR.

28. A DNA molecule according to Claim 24 wherein,
for the encoded amino acid sequence, the corresponding
wild-type luciferase is selected from the group
20 consisting of LucPplGR, LucPplyG, LucPplyE, and LucPplOR.

29. A DNA molecule according to Claim 25 wherein,
for the encoded amino acid sequence, the corresponding
wild-type luciferase is selected from the group
consisting of LucPplGR, LucPplyG, LucPplyE, and LucPplOR.

25 30. A DNA molecule according to Claim 26 wherein,
for the encoded amino acid sequence, the corresponding
wild-type luciferase is LucPplGR.

31. A DNA molecule according to Claim 27 wherein,
for the encoded amino acid sequence, the corresponding
30 wild-type luciferase is LucPplGR.

32. A DNA molecule according to Claim 28 wherein,
for the encoded amino acid sequence, the corresponding
wild-type luciferase is LucPplGR.

33. A DNA molecule according to Claim 29 wherein,
35 for the encoded amino acid sequence, the corresponding
wild-type luciferase is LucPplGR.

34. A DNA molecule according to Claim 30 wherein the encoded mutant luciferase is selected from the group consisting of LucPplGR-R₂₁₅H, -R₂₁₅G, -R₂₁₅T, -R₂₁₅M, -R₂₁₅P, -R₂₁₅A, -R₂₁₅L, -R₂₂₃L, -R₂₂₃Q, -R₂₂₃M, -R₂₂₃H, -V₂₂₄I, -V₂₂₄S, -V₂₂₄F, 5 -V₂₂₄Y, -V₂₂₄L, -V₂₂₄H, -V₂₂₄G, -V₂₃₂E, -V₂₃₆H, -V₂₃₆W, -Y₂₃₇S, -Y₂₃₇C, -L₂₃₈R, -L₂₃₈M, -L₂₃₈Q, -L₂₃₈S, -L₂₃₈D, -H₂₄₂A, -F₂₄₄L, -G₂₄₅S, -G₂₄₅E, -S₂₄₇H, -S₂₄₇T, -S₂₄₇Y, -S₂₄₇F, -I₂₄₈R, -I₂₄₈V, -I₂₄₈F, -I₂₄₈T, -I₂₄₈S, -I₂₄₈N, -H₃₄₈N, -H₃₄₈Q, -H₃₄₈E, -H₃₄₈C, -S₂₄₇F/F₂₄₆L, -S₂₄₇F/I₂₄₈C, -S₂₄₇F/I₂₄₈T, -V₂₂₄F/R₂₁₅G, -V₂₂₄F/R₂₁₅T, -V₂₂₄F/R₂₁₅V, -V₂₂₄F/R₂₁₅P, 10 -V₂₂₄F/P₂₂₂S, -V₂₂₄F/Q₂₂₇E, -V₂₂₄F/L₂₃₈V, -V₂₂₄F/L₂₃₈T, -V₂₂₄F/S₂₄₇G, -V₂₂₄F/S₂₄₇H, -V₂₂₄F/S₂₄₇T, and -V₂₂₄F/S₂₄₇F.

INTERNATIONAL SEARCH REPORT

Inter. application No.
PCT/US95/00108

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) :C12N 9/02, 15/53 US CL :435/189; 536/23.2 According to International Patent Classification (IPC) or to both national classification and IPC														
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/189, 172.3, 320.1, 252.3, 252.33; 536/23.2 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) Please See Extra Sheet.														
C. DOCUMENTS CONSIDERED TO BE RELEVANT														
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.												
X	FEBS Letters, Volume 307, No. 2, issued July 1992, G. Sala-Newby et al., "Engineering Firefly Luciferase as an Indicator of Cyclic AMP-Dependent Protein Kinase in Living Cells", pages 241-244, see entire document.	1, 2, 5, 6, 18, 19, 22, 23												
X	BIOCHEMICAL JOURNAL, Volume 279, issued November 1991, G. Sala-Newby et al., "Engineering a Bioluminescent Indicator for Cyclic AMP-Dependent Protein Kinase", pages 727-732, see entire document.	1, 2, 5, 6, 18, 19, 22, 23												
A	PROTEIN ENGINEERING, Volume 4, No. 6, issued August 1991, N. Kajiya et al., "Isolation and Characterization of Mutants of Firefly Luciferase Which Produce Different Colors of Light", pages 691-693.	1-34												
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.														
<table border="0"> <tr> <td>* Special categories of cited documents:</td> <td>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td> </tr> <tr> <td>"A" document defining the general state of the art which is not considered to be of particular relevance</td> <td>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td> </tr> <tr> <td>"E" earlier document published on or after the international filing date</td> <td>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td> </tr> <tr> <td>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td> <td>"G" document member of the same patent family</td> </tr> <tr> <td>"O" document referring to an oral disclosure, use, exhibition or other means</td> <td></td> </tr> <tr> <td>"P" document published prior to the international filing date but later than the priority date claimed</td> <td></td> </tr> </table>			* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	"E" earlier document published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"G" document member of the same patent family	"O" document referring to an oral disclosure, use, exhibition or other means		"P" document published prior to the international filing date but later than the priority date claimed	
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Date of the actual completion of the international search 05 APRIL 1995		Date of mailing of the international search report 17 APR 1995												
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230		Authorized officer <i>Rebecca Prouty</i> REBECCA PROUTY Telephone No. (703) 308-0196												

INTERNATIONAL SEARCH REPORTInter. .onal application No.
PCT/US95/00108**C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	JOURNAL OF BIOLUMINESCENCE AND CHEMILUMINESCENCE, Volume 5, issued April 1990, K.V. Wood, "Luc Genes: Introduction of Colour Into Bioluminescence Assays", pages 107-114.	1-34
A	JOURNAL OF BIOLUMINESCENCE AND CHEMILUMINESCENCE, Volume 4, issued July 1989, K.V. Wood et al., "Introduction to Beetle Luciferases and Their Applications", pages 289-301.	1-34
A	JOURNAL OF BIOLUMINESCENCE AND CHEMILUMINESCENCE, Volume 4, issued July 1989, K.V. Wood et al., "Bioluminescent Click Beetles Revisited", pages 31-39.	1-34
A	SCIENCE, Volume 244, issued 12 May 1989, K.V. Wood et al., "Complementary DNA Coding Click Betle Luciferases Can Elicit Bioluminescence of Different Colors", pages 700-702.	1-34

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/00108

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, MEDLINE, BIOSIS, LIFESCI, EMBASE, WPI, BIOTECHDS, CA

search terms: luciferase#, muta? or modif?, gene# or sequence#, beetle# or firefl?, pyrophorus or plagiophthalmus, photinus or luciola